P. Gamble

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/251,073

DATE: 05/01/2001
TIME: 16:31:12

Input Set : N:\Crf3\RULE60\09251073.txt
Output Set: N:\CRF3\05012001\I251073.raw

SEQUENCE LISTING
```
 4  (1) GENERAL INFORMATION:
 6      (i) APPLICANT: Lobb, Roy R.; Burkly, Linda C.
 8     (ii) TITLE OF INVENTION: Treatment for Asthma with VLA-4 Blocking
 9                            Agents
11    (iii) NUMBER OF SEQUENCES: 13
13     (iv) CORRESPONDENCE ADDRESS:
14          (A) ADDRESSEE: LAHIVE & COCKFIELD, LLP
15          (B) STREET: 28 State Street
16          (C) CITY: Boston                    ENTERED
17          (D) STATE: Massachusetts
18          (E) COUNTRY: USA
19          (F) ZIP: 02109
21      (v) COMPUTER READABLE FORM:
22          (A) MEDIUM TYPE: Floppy disk
23          (B) COMPUTER: IBM PC compatible
24          (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25          (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
27     (vi) CURRENT APPLICATION DATA:
28          (A) APPLICATION NUMBER: US/09/251,073
29          (B) FILING DATE: 16-Feb-1999
48    (vii) PRIOR APPLICATION DATA:
32          (A) APPLICATION NUMBER: 08/822,830
34          (B) FILING DATE:
37          (A) APPLICATION NUMBER: US 08/374,331
38          (B) FILING DATE: 18-JAN-1995
41          (A) APPLICATION NUMBER: US 08/256,631
42          (B) FILING DATE: 12-JUL-1994
45          (A) APPLICATION NUMBER: PCT/US93/00030
46          (B) FILING DATE: 12-JAN-1993
49          (A) APPLICATION NUMBER: 07/821,768
50          (B) FILING DATE: 13-JAN 1992
52   (viii) ATTORNEY/AGENT INFORMATION:
53          (A) NAME: Myers, Louis (PLM)
54          (B) REGISTRATION NUMBER: 35,965
55          (C) REFERENCE/DOCKET NUMBER: BGP-021USCN
57     (ix) TELECOMMUNICATION INFORMATION:
58          (A) TELEPHONE: (617)227-7400
59          (B) TELEFAX: (617)742-4214
62  (2) INFORMATION FOR SEQ ID NO: 1:
64      (i) SEQUENCE CHARACTERISTICS:
65          (A) LENGTH: 363 base pairs
66          (B) TYPE: nucleic acid
67          (C) STRANDEDNESS: single
68          (D) TOPOLOGY: linear
70     (ii) MOLECULE TYPE: cDNA
73     (ix) FEATURE:
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C--> 28
C--> 29

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74          (A) NAME/KEY: CDS
75          (B) LOCATION: 1..363
77     (ix) FEATURE:
78          (A) NAME/KEY: misc_feature
79          (B) LOCATION: 1
80          (D) OTHER INFORMATION: /note= "pBAG159 insert: HP1/2 heavy
81 chain variable region"
84     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
86 GAR GTC AAA CTG CAG CAG TCT GGG GCA GAG CTT GTG AAG CCA GGG GCC        48
87 Glu Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
88   1           5                   10                  15
90 TCA GTC AAG TTG TCC TGC ACA GCT TCT GGC TTC AAC ATT AAA GAC ACC        96
91 Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr
92              20                  25                  30
94 TAT ATG CAC TGG GTG AAG CAG AGG CCT GAA CAG GGC CTG GAG TGG ATT       144
95 Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
96         35                  40                  45
98 GGA AGG ATT GAT CCT GCG AGT GGC GAT ACT AAA TAT GAC CCG AAG TTC       192
99 Gly Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe
100       50                  55                  60
102 CAG GTC AAG GCC ACT ATT ACA GCG GAC ACG TCC TCC AAC ACA GCC TGG      240
103 Gln Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp
104  65                  70                  75                  80
106 CTG CAG CTC AGC AGC CTG ACA TCT GAG GAC ACT GCC GTC TAC TAC TGT      288
107 Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
108             85                  90                  95
110 GCA GAC GGA ATG TGG GTA TCA ACG GGA TAT GCT CTG GAC TTC TGG GGC      336
111 Ala Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly
112             100                 105                 110
114 CAA GGG ACC ACG GTC ACC GTC TCC TCA                                 363
115 Gln Gly Thr Thr Val Thr Val Ser Ser
116         115                 120
118 (2) INFORMATION FOR SEQ ID NO: 2:
120     (i) SEQUENCE CHARACTERISTICS:
121          (A) LENGTH: 121 amino acids
122          (B) TYPE: amino acid
123          (D) TOPOLOGY: linear
125    (ii) MOLECULE TYPE: protein
127    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
129 Glu Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
130   1           5                   10                  15
132 Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr
133             20                  25                  30
135 Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
136         35                  40                  45
138 Gly Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe
139       50                  55                  60
141 Gln Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp
142  65                  70                  75                  80
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144 Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
145   85   90   95
147 Ala Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly
148   100   105   110
150 Gln Gly Thr Thr Val Thr Val Ser Ser
151   115   120
153 (2) INFORMATION FOR SEQ ID NO: 3:
155   (i) SEQUENCE CHARACTERISTICS:
156   (A) LENGTH: 318 base pairs
157   (B) TYPE: nucleic acid
158   (C) STRANDEDNESS: single
159   (D) TOPOLOGY: linear
161   (ii) MOLECULE TYPE: cDNA
164   (ix) FEATURE:
165   (A) NAME/KEY: CDS
166   (B) LOCATION: 1..318
167   (D) OTHER INFORMATION: /note= "HP1/2 light chain variable
168 region"
170   (ix) FEATURE:
171   (A) NAME/KEY: misc_feature
172   (B) LOCATION: 1
173   (D) OTHER INFORMATION: /note= "pBAG172 insert: HP1/2 light
174 chain variable region"
177   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
179 AGT ATT GTG ATG ACC CAG ACT CCC AAA TTC CTG CTT GTT TCA GCA GGA   48
180 Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly
181 1   5   10   15
183 GAC AGG GTT ACC ATA ACC TGC AAG GCC AGT CAG AGT GTG ACT AAT GAT   96
184 Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Thr Asn Asp
185   20   25   30
187 GTA GCT TGG TAC CAA CAG AAG CCA GGG CAG TCT CCT AAA CTG CTG ATA   144
188 Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
189   35   40   45
191 TAT TAT GCA TCC AAT CGC TAC ACT GGA GTC CCT GAT CGC TTC ACT GGC   192
192 Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
193   50   55   60
195 AGT GGA TAT GGG ACG GAT TTC ACT TTC ACC ATC AGC ACT GTG CAG GCT   240
196 Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ala
197 65   70   75   80
199 GAA GAC CTG GCA GTT TAT TTC TGT CAG CAG GAT TAT AGC TCT CCG TAC   288
200 Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln Asp Tyr Ser Ser Pro Tyr
201   85   90   95
203 ACG TTC GGA GGG GGG ACC AAG CTG GAG ATC   318
204 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
205   100   105
208 (2) INFORMATION FOR SEQ ID NO: 4:
210   (i) SEQUENCE CHARACTERISTICS:
211   (A) LENGTH: 106 amino acids
212   (B) TYPE: amino acid

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```
213              (D) TOPOLOGY: linear
215      (ii) MOLECULE TYPE: protein
217      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
219 Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly
220  1               5                  10                  15
222 Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Thr Asn Asp
223             20                  25                  30
225 Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
226         35                  40                  45
228 Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
229     50                  55                  60
231 Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ala
232 65                  70                  75                  80
234 Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln Asp Tyr Ser Ser Pro Tyr
235                 85                  90                  95
237 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
238  ·              100                 105
241 (2) INFORMATION FOR SEQ ID NO: 5:
243      (i) SEQUENCE CHARACTERISTICS:
244              (A) LENGTH: 1347 base pairs
245              (B) TYPE: nucleic acid
246              (C) STRANDEDNESS: single
247              (D) TOPOLOGY: linear
249      (ii) MOLECULE TYPE: cDNA
C--> 257              (A) CHROMOSOME/SEGMENT: VCAM-1 gene segment
252      (ix) FEATURE:
253              (A) NAME/KEY: CDS
254              (B) LOCATION: 1..1338
256      (ix) FEATURE:
264      (ix) FEATURE:
265              (A) NAME/KEY: Hinge region
266              (B) LOCATION: 220..229
267              (D) OTHER INFORMATION: This portion of the sequence
268 corresponds, in part, to Fig. 12A in PCT/US92/02050 and
269 represents the hinge region of Human IgG1 heavy chain
270 constant region.
272      (ix) FEATURE:
273              (A) NAME/KEY: Heavy chain constant region 2
274              (B) LOCATION: 230..338
275        -     (D) OTHER INFORMATION: This portion of the sequence
276 corresponds, in part, to Fig. 12A in PCT/US92/02050 and
277 represents the heavy chain constant region 2 of Human
278 IgG1 heavy chain constant region.
280  - - -(ix) FEATURE:
281              (A) NAME/KEY: Heavy chain constant region 3
282              (B) LOCATION: 339..446
283              (D) OTHER INFORMATION: This portion of the sequence
284 corresponds, in part, to Fig. 12A in PCT/US92/02050 and
285 represents the heavy chain constant region 3 of Human
```

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```
286 IgG1 heavy chain constant region.
289     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
291 ATG CCT GGG AAG ATG GTC GTG ATC CTT GGA GCC TCA AAT ATA CTT TGG        48
292 Met Pro Gly Lys Met Val Val Ile Leu Gly Ala Ser Asn Ile Leu Trp
W--> 293 110               115               120               125
295 ATA ATG TTT GCA GCT TCT CAA GCT TTT AAA ATC GAG ACC ACC CCA GAA        96
296 Ile Met Phe Ala Ala Ser Gln Ala Phe Lys Ile Glu Thr Thr Pro Glu
W--> 297           130               135               140
299 TCT AGA TAT CTT GCT CAG ATT GGT GAC TCC GTC TCA TTG ACT TGC AGC       144
300 Ser Arg Tyr Leu Ala Gln Ile Gly Asp Ser Val Ser Leu Thr Cys Ser
W--> 301           145               150               155
303 ACC ACA GGC TGT GAG TCC CCA TTT TTC TCT TGG AGA ACC CAG ATA GAT       192
304 Thr Thr Gly Cys Glu Ser Pro Phe Phe Ser Trp Arg Thr Gln Ile Asp
W--> 305           160               165               170
307 AGT CCA CTG AAT GGG AAG GTG ACG AAT GAG GGG ACC ACA TCT ACG CTG       240
308 Ser Pro Leu Asn Gly Lys Val Thr Asn Glu Gly Thr Thr Ser Thr Leu
W--> 309       175               180               185
311 ACA ATG AAT CCT GTT AGT TTT GGG AAC GAA CAC TCT TAC CTG TGC ACA       288
312 Thr Met Asn Pro Val Ser Phe Gly Asn Glu His Ser Tyr Leu Cys Thr
W--> 313 190               195               200               205
315 GCA ACT TGT GAA TCT AGG AAA TTG GAA AAA GGA ATC CAG GTG GAG ATC       336
316 Ala Thr Cys Glu Ser Arg Lys Leu Glu Lys Gly Ile Gln Val Glu Ile
W--> 317           210               215               220
319 TAC TCT TTT CCT AAG GAT CCA GAG ATT CAT TTG AGT GGC CCT CTG GAG       384
320 Tyr Ser Phe Pro Lys Asp Pro Glu Ile His Leu Ser Gly Pro Leu Glu
W--> 321           225               230               235
323 GCT GGG AAG CCG ATC ACA GTC AAG TGT TCA GTT GCT GAT GTA TAC CCA       432
324 Ala Gly Lys Pro Ile Thr Val Lys Cys Ser Val Ala Asp Val Tyr Pro
W--> 325           240               245               250
327 TTT GAC AGG CTG GAG ATA GAC TTA CTG AAA GGA GAT CAT CTC ATG AAG       480
328 Phe Asp Arg Leu Glu Ile Asp Leu Leu Lys Gly Asp His Leu Met Lys
W--> 329       255               260               265
331 AGT CAG GAA TTT CTG GAG GAT GCA GAC AGG AAG TCC CTG GAA ACC AAG       528
332 Ser Gln Glu Phe Leu Glu Asp Ala Asp Arg Lys Ser Leu Glu Thr Lys
W--> 333 270               275               280               285
335 AGT TTG GAA GTA ACC TTT ACT CCT GTC ATT GAG GAT ATT GGA AAA GTT       576
336 Ser Leu Glu Val Thr Phe Thr Pro Val Ile Glu Asp Ile Gly Lys Val
W--> 337           290               295               300
339 CTT GTT TGC CGA GCT AAA TTA CAC ATT GAT GAA ATG GAT TCT GTG CCC       624
340 Leu Val Cys Arg Ala Lys Leu His Ile Asp Glu Met Asp Ser Val Pro
W--> 341           305               310               315
343 ACA GTA AGG CAG GCT GTA AAA GAA TTG CAA GTC GAC AAA ACT CAC ACA       672
344 Thr Val Arg Gln Ala Val Lys Glu Leu Gln Val Asp Lys Thr His Thr
W--> 345       320               325               330
347 TGC CCA CCG TGC CCA GCA CCT GAA CTC CTG GGG GGA CCG TCA GTC TTC       720
348 Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
W--> 349       335               340               345
351 CTC TTC CCC CCA AAA CCC AAG GAC ACC CTC ATG ATC TCC CGG ACC CCT       768
352 Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
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VERIFICATION SUMMARY
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Input Set : N:\Crf3\RULE60\09251073.txt
Output Set: N:\CRF3\05012001\I251073..raw

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:257 M:220 C: Keyword misspelled or invalid format, [(A) CHROMOSOME/SEGMENT:]
L:257 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=5
L:293 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:297 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:301 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:305 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:309 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:313 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:317 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:321 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:325 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:329 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:333 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:337 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:341 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:345 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:349 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:353 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:357 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:361 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:365 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:369 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:373 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:377 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:381 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:385 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:389 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:393 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:397 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:401 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5